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Quantitative Assessment of the Small Bowel Motility with Negative Mutual Information in Cine-MRI Sequences

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Abstract

Cine-MRI provides a well tolerated non-invasive method for the quantitative assessment of small bowel motility. The quantitative assessment of the small bowel motility reveals important information for the functional analysis of the small bowel. Traditionally the quantitative assessment is accomplished by detecting the peristaltic frequency of a specific small bowel segment within MRI sequences. Negative mutual information is proposed to assess the small bowel motility. A simulation of the small bowel motility is implemented, which proves that the proposed method can be utilized for the quantitative assessment. Experimental results demonstrate the accuracy of proposed method.

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Keywords: small bowel; motility; simulation; MRI; negative mutual information;

1. Introduction

Small bowel's function is complex and physiological measurements are difficult due to its unpredictable movements and the complex structure [1] formed by the convoluted bowel. Furthermore small bowel disorders [2] and dysfunction will affect its normal peristaltic frequency. Quantitative assessment for small bowel motility would be informative for the diagnosis of small bowel diseases. Moreover some medicine will accelerate small bowel motility, whereas some will decelerate its motility. Qualitative and quantitative assessment for small bowel motility would give direct evidence of these medicines' effects.

Cine-MRI [3] provides a well tolerated non-invasive method [4] for the qualitative and quantitative assessment of small bowel motility. Cine-MRI can observe peristaltic contraction of small bowel and

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allows dynamic analysis of its moving structures under physiological conditions. There have been some studies concerning the analysis of small bowel motility with MRI, which focused on the peristaltic frequency of a specific small bowel segment. Froehlich and et al. [5] proposed a method to evaluate peristaltic motion by manually measuring intra-luminal diameters of selected small bowel segments on each MR Imaging of MRI sequences. Ailiani and et al. [6] used dynamic MRI for the quantitative analysis of peristaltic and segmental motion in vivo in the rat small intestine. With the three-dimensional live wire and directional dynamic gradient vector flow snakes, they segmented out the jejunum region and computed the diameter at fixed location for a quantitative analysis for the small bowel motility. Our group also proposed assessment strategy for small bowel motility with traditional fast marching method [7] and orientation adaptive fast marching method [8] via specific small bowel segments.

Previously mentioned quantitative assessment for the small bowel motility with MRI is to pick up a specific small bowel segment and record the variation of its intra-luminal diameter in a certain period. According to the variation of its intra-luminal diameter, small bowel's peristaltic frequency can be calculated out. However the peristaltic frequency of this specific segment can not sufficiently represent the peristaltic frequency of the whole small bowel loops. It is proposed that the difference between adjacent MR images (short as DBAM) in a ROI (region of interest) is utilized for the quantitative assessment of small bowel motility.

2. MRI sequence acquisition and analysis

Cine-MR imaging was performed in three healthy volunteers without abdominal symptoms after 8 hours of fasting with transoral administration of 1500mL of non-absorbable fluid prior to scanning. Cine-MR imaging was performed with 1.5-T MR machine using 12-channel body array coil. The balanced steady-state free precession imaging, FIESTA sequence (TR/TE=3.4/1.2msec, Flip angle=75 degree, acquisition time per image=0.5 sec) was utilized and the area of 45cm x 45cm was imaged to cover the entire loops of the small bowel. Ten mm-thick coronal images were obtained at every 0.5 seconds for 30 seconds during breath hold at 0, 15, 30 ,45, and 60 minutes after oral intake of contrast. Totally 9 sequences [9] were acquired to verify the proposed detection method.

To prove the feasibility of the proposed method, the characteristics of Cine-MR images should be concerned. A sequence was randomly selected from previously acquired sequences. The positions of two ROI were defined by an experienced radiologist at the first MR image of the whole sequence. On each image of the sequence, two ROI were automatically drawn and analyzed. The first four MR images were picked up and the ROI on these images were cropped and enlarged as shown in Fig.1.

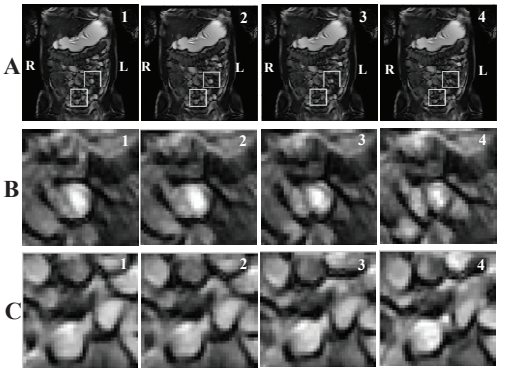

Fig. 1. (a) Original MR Images with ROI; (b) Enlarged upper right ROI; (c) Enlarged lower right ROI.

The row A of Fig. 1 shows original adjacent MR images with ROI. The row B is the enlarged part of the upper left ROI and the row C is the enlarged part of the lower right ROI. It is clearly demonstrated by these images that the intensity in ROI varies according to the small bowel motility, which result in our assumption that the DBAM can be utilized to quantitatively assess the small bowel motility. To verify the feasibility of DBAM, it should be discussed that the relationship among DBAM, MR images' intensity and the small bowel peristaltic frequency.

3. DBAM in negative mutual information

In our previous study [10], the relationship between the value of DBAM and the small bowel peristaltic frequency is discussed. It was proved that the value of DBAM has positive linear correlation with the peristaltic frequency.

We previously obtained DBAM value by calculating the sum of pixel intensity difference between adjacent images using the following formula:

$$I_{diff} = \sum_{x=1}^{256}\sum_{y=1}^{256}\sqrt{\left(I_t(x,y)/65536 - I_{t-1}(x,y)/65536\right)^2} \quad (1)$$

where $I_t(x,y)$ is the pixel intensity of the current image and $I_{t-1}(x,y)$ is the corresponding pixel intensity of the previous image. It is proved in our previous study that the value of DBAM I_{diff} shows a positive linear correlation with the simulated small bowel peristaltic frequency. Furthermore, a normalized I_{diff} was proposed as follows:

$$I_{ndiff} = \sum_{x=1}^{256}\sum_{y=1}^{256}\sqrt{\left(I_{t+1}(x,y)/I_{\max} - I_t(x,y)/I_{\max}\right)^2} \quad (2)$$

where $I_{\max}$ means the largest sum of the intensity from all MR images in a sequence. Because the value of $I_{\max}$ is unique in one sequence, it can be used as the normalization factor. Although normalized DBAM has positive linear correlation with small bowel peristaltic frequency, the pixel intensity difference is sensitive to the change of pixel intensity. Thus the pixel intensity difference is substituted for modified negative mutual information, which determines the value of DBAM. The relationship between the negative mutual information determined value of DBAM and the small bowel peristaltic frequency should be discussed.

3.1. Correlation between DBAM and small bowel peristaltic frequency

It was assumed that the value of DBAM should have positive linear correlation with the peristaltic frequency. Four simulated sequences as shown in Figure 2 were generated to verify this assumption.

In every sequence, there are 150 images and each image is in a size of 256*256 pixels. In our real Cine-MRI sequences, acquisition time per image is half a second. Thus these 150 images sequences simulate four 75-second Cine-MRI sequences. The images of these sequences were generated to simulate a ROI of small bowel loops. Three cycles were put on these images, which simulate three small bowel segments.

It is the radiuses of three cycles were set to vary periodically following a sine function. For different sequence, radiuses vary in different frequencies that simulate different small bowel peristaltic frequencies. The simulated peristaltic frequencies are set as five times per minute (1/12 Hz), ten times per minute (1/6 Hz), twenty times per minute (1/3 Hz) and thirty times per minute (1/2 Hz) as defined as follows:

$$r = r0*(\sin(2\pi*(f)*c+2)+p),\ f=1/12,\ 1/6,\ 1/3,\ 1/2,\ p=2,4,6. \quad (3)$$

where r0 is a predefined radius, c is a constant and p is the phase of this small bowel segment. According to the change of radiuses, the areas of three cycles also vary periodically. A cycle's expansion represents that there are some material pass through this small bowel segment.

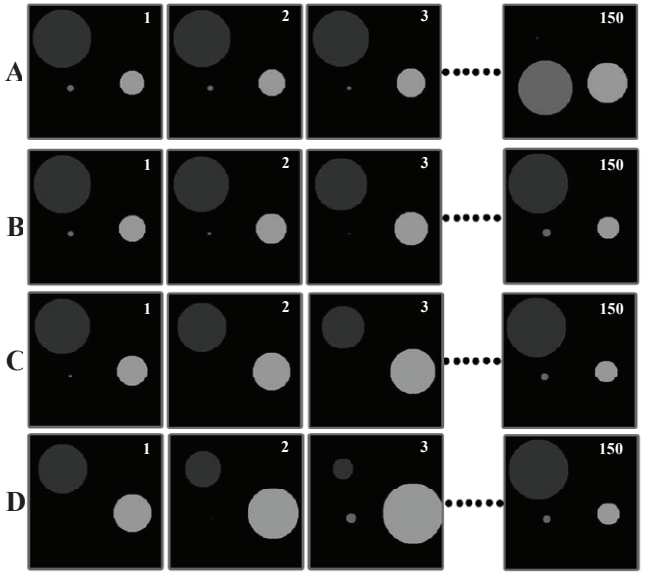

Fig. 2. (a) f=5times/m; (b) f=10 times/m; (c) f=20 times/m; (d) f=30 times/m.

In reality with the movement of this material, the intensity of small bowel segments will change accordingly. Thus to approach the reality and simulate the movement of this material, three cycles were set in different intensity 50, 100 and 150. Furthermore the variation of three cycles' radiuses is also set in different phases.

For previous generated four sequences, the DBAM was obtained by calculating the proposed negative mutual information. The proposed negative mutual information is different with Parzen proposed one [11]. The negative mutual information with Parzen window is as follows:

$$MI_n(\mu) = -\sum_{k\in L_R}\sum_{l\in L_T} p(l,k;\mu)\log_2\frac{p(l,k;\mu)}{p_R(k;\mu)\cdot p_T(l;\mu)} \tag{4}$$

Because the high computing complexity of Parzen proposed negative mutual information does not suit for our application, we propose another form of negative mutual information by modifying normalized mutual information. The normalized mutual information proposed by Studholme [12] is as follows:

$$NMI(X,Y) = \frac{H(X)+H(Y)}{H(X,Y)} \tag{5}$$

where $H(X)$ is the entropy of an image X, $H(Y)$ is the entropy of another image Y and $H(X,Y)$ is the joint entropy of image X and image Y. The normalized mutual information is used as the measure of similarity between two images. To determine the value of DBAM, a dissimilarity metrics is needed. Because the value of normalized mutual information ranges from 1 to 2, we propose the negative mutual information as follows:

$$MI_n(X,Y) = 2 - \frac{H(X)+H(Y)}{H(X,Y)} \quad (6)$$

The proposed negative mutual information ranges from 0 to 1, which can measure dissimilarity between two images.

In previous generated four sequences as shown in Figure 2, the DBAM was obtained by calculating the negative mutual information between adjacent images using proposed formula as follows:

$$MI_n(X_t, X_{t-1}) = 2 - \frac{H(X_t)+H(X_{t-1})}{H(X_t, X_{t-1})} \quad (7)$$

where X_t is current simulated MR image and X_{t-1} is its previous MR image. After calculating the negative mutual information between two images from all 150 images of a sequence, we can get 149 values for MI_n and their average can be calculated out. For those four different sequences with different frequencies, four average values are marked on Figure 3 and a fitting line is drawn.

It is clearly shown in Figure 3 that the MI_n determined value of DBAM shows a positive linear correlation with the simulated small bowel peristaltic frequency, which proved our assumption. Furthermore, it should be investigated for the relationship among MI_n determined value of DBAM, the intensity of small bowel segments and small bowel peristaltic frequencies.

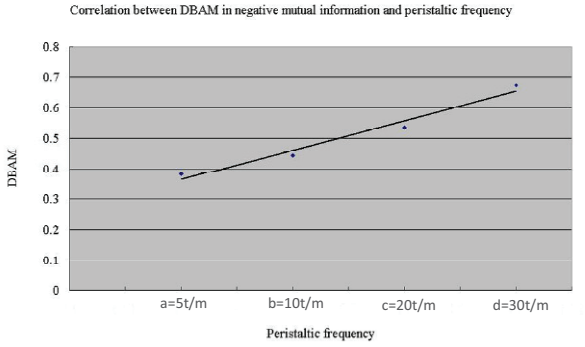

Fig. 3. Correlation between DBAM with the mutual information and small bowel peristaltic frequencies

3.2. Relationship among the value of DBAM, the intensity and the peristaltic frequency

To investigate the relationship among the value of DBAM, the intensity of small bowel segments and the peristaltic frequency, twenty more sequences were generated. As shown in Figure 4, simulated small bowel segments in these sequences have same intensity in the same row and different simulated peristaltic frequencies in different columns. The purpose for these arrangements is to discuss the intensity of small bowel segments and its peristaltic frequency separately.

It is demonstrated in Figure 4, images in these twenty sequences have three simulated small bowel segments, which have the same intensity 50 (sequence 1 to 4), 100 (sequence 5 to 8), 150 (sequence 9 to 12), 200 (sequence 13 to 16) and 250 (sequence 17 to 20). Furthermore for sequences in different columns, they have four different peristaltic frequencies, which are 5 times per minute (sequence 1, 5, 9, 13 to 17), 10 times per minute (sequence 2, 6, 10, 14 to 18), 20 times per minute (sequence 3, 7, 11, 15 to 19) and 30 times per minute (sequence 4, 8, 12, 16 to 20).

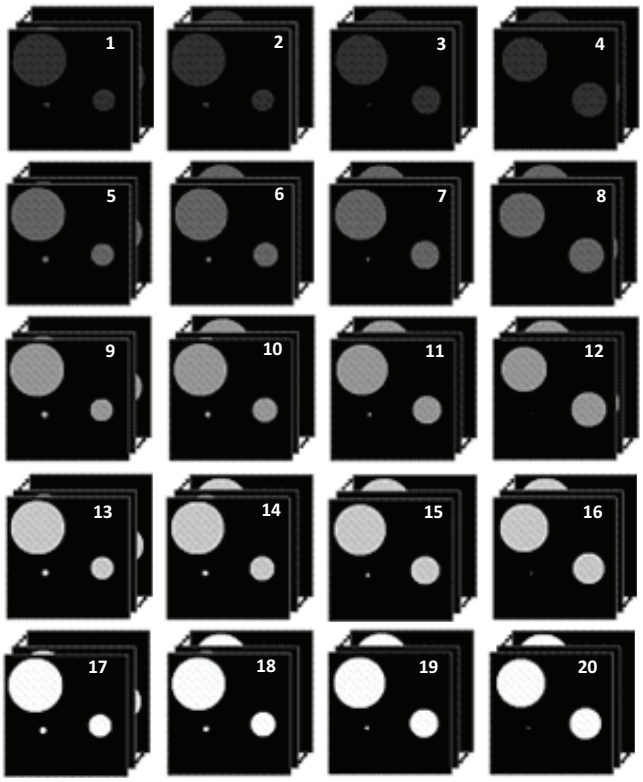

Fig. 4. Twenty sequences with different intensities and different peristaltic frequencies

It is demonstrated in Figure 4, images in these twenty sequences have three simulated small bowel segments, which have the same intensity 50 (sequence 1 to 4), 100 (sequence 5 to 8), 150 (sequence 9 to 12), 200 (sequence 13 to 16) and 250 (sequence 17 to 20). Furthermore for sequences in different columns, they have four different peristaltic frequencies, which are 5 times per minute (sequence 1, 5, 9, 13 to 17), 10 times per minute (sequence 2, 6, 10, 14 to 18), 20 times per minute (sequence 3, 7, 11, 15 to 19) and 30 times per minute (sequence 4, 8, 12, 16 to 20).The MI_n determined value of DBAM shows a positive linear correlation with the simulated small bowel peristaltic frequency. Furthermore it is assumed that the MI_n determined value of DBAM should have no relationship with the intensity of small bowel segments. Thus in previous generated twenty sequences, the MI_n determined value of DBAM were calculated for each sequence. The negative mutual information between two images from all 150 images of a sequence, we can get 149 values for MI_n and their average can be calculated out. All the values are marked on Figure 5 and the horizontal axis is the simulated small bowel peristaltic frequencies: five times per minute (5t/m), ten times per minute (10t/m), twenty times per minute (20t/m) and thirty times per minute (30t/m). The vertical axis is the value of MI_n determined value of DBAM.

It is clearly demonstrated in Figure 5 that fitting lines for different intensity coincided with each other. Even for different intensities the MI_n determined value of DBAM has the same value in the same peristaltic frequency. A conclusion can be safely drawn that MI_n determined value of DBAM only has positive linear correlation with small bowel peristaltic frequency and has no relationship with the intensity of small bowel segments. Thus the MI_n determined value of DBAM, DBAM in negative mutual information, can be utilized to quantitatively assess the motility of the small bowel. The proposed DBAM

in negative mutual information will be testified in real small bowel Cine-MR sequences. The performance comparison between DBAM in intensity difference and DBAM in negative mutual information will be demonstrated in next section.

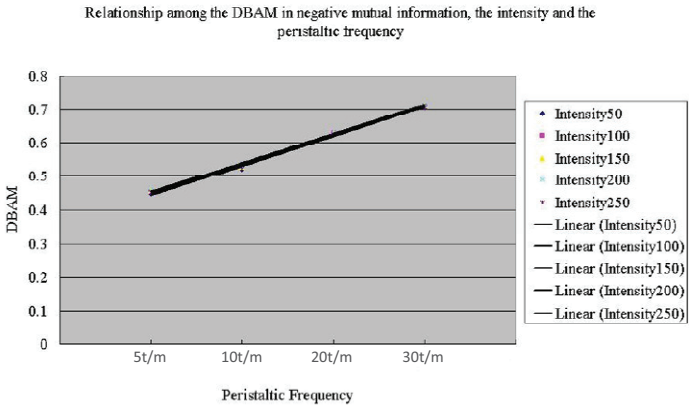

Fig. 5. Relationship among the DBAM with mutual information, the intensities and the peristaltic frequencies

4. Experimental results

With the 9 sequences acquired in section Ⅱ, DBAM in different methods were calculated for these sequences. Figure 6 shows the first MR image of these 9 sequences, on which two ROI were marked by the experienced radiologist. Followed the real body positions of volunteers, the ROI was defined as ROIL (ROI Left) and ROIR (ROI right). That is, within the radiologist marked ROI in the first MR image, DBAM were calculated for the whole sequence.

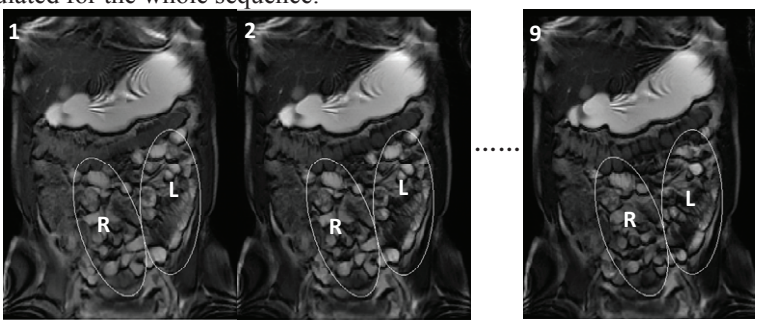

Fig. 6. Determination of the ROI in the DBAM method.

The peristaltic frequencies for ROIL and ROIR were first manually measured by two experienced radiologists. The average of their manual measuring results is the golden standard to testify the accuracy of DBAM with different methods. After the DBAM value was determined by intensity difference and negative mutual information, the peristaltic frequencies were calculated by FFT (Fast Fourier Transform). These peristaltic frequencies were represented in peristaltic times per minute. The results for ROIL and ROIR are recorded in Table I and Table II respectively.

Table 1. ROIL DBAM with different methods

Sequences	ROIL		
	Manual	*Intensity difference*	*Negative mutual info.*
Sequence 1	6t/m	6.8 t/m	6 t/m
Sequence 2	8 t/m	9.3 t/m	8.5 t/m
Sequence 3	12 t/m	13.6 t/m	12.7 t/m
Sequence 4	8 t/m	8.9 t/m	8 t/m
Sequence 5	11 t/m	12.2 t/m	11.5 t/m
Sequence 6	15 t/m	16.6 t/m	15.8 t/m
Sequence 7	7 t/m	8 t/m	7 t/m
Sequence 8	10 t/m	11.4 t/m	10.4 t/m
Sequence 9	14 t/m	15.3 t/m	14.6 t/m

Table 2. ROIR DBAM with different methods.

Sequences	ROIR		
	Manual	*Intensity difference*	*Negative mutual info.*
Sequence 1	7 t/m	8.1 t/m	7.4 t/m
Sequence 2	8 t/m	9.3 t/m	8.5 t/m
Sequence 3	13 t/m	14.5 t/m	13.6 t/m
Sequence 4	8 t/m	9.3 t/m	8.7 t/m
Sequence 5	10 t/m	11.1t/m	10.4 t/m
Sequence 6	15 t/m	16.3t/m	15.4 t/m
Sequence 7	7 t/m	7.9 t/m	7 t/m
Sequence 8	10 t/m	11.3 t/m	10.5 t/m
Sequence 9	13 t/m	14.6t/m	13.8 t/m

From Table I and Table II, we can see that the peristaltic times calculated by DBAM with intensity difference and negative mutual information both larger than the manual measuring results, but they are still in the reasonable range. For volunteer 1, the errors in ROIL calculated by intensity difference ranged from +0.8t/m to +1.6t/m and the errors calculated by negative mutual information ranged from 0t/m to +0.7t/m in Sequence 1, Sequence 2 and Sequence 3; For volunteer 2, the errors in ROIL calculated by intensity difference ranged from +0.9t/m to +1.6t/m and the errors calculated by negative mutual information ranged from 0t/m to +0.8t/m in Sequence 4, Sequence 5 and Sequence 6; For volunteer 3, the errors in ROIL calculated by intensity difference ranged from +1t/m to +1.6t/m and the errors calculated by negative mutual information ranged from 0t/m to +0.6t/m in Sequence 7, Sequence 8 and Sequence 9.

In Table II, the measuring results for ROIR are recorded. For volunteer 1, the errors in ROIR calculated by intensity difference ranged from +1.1t/m to +1.5t/m and the errors calculated by negative mutual information ranged from 0.4t/m to +0.6t/m in Sequence 1, Sequence 2 and Sequence 3; For volunteer 2, the errors in ROIR calculated by intensity difference ranged from +1.1t/m to +1.3t/m and the errors calculated by negative mutual information ranged from 0.4t/m to +0.7t/m in Sequence 4, Sequence 5 and Sequence 6; For volunteer 3, the errors in ROIR calculated by intensity difference ranged from

+0.9t/m to +1.6t/m and the errors calculated by negative mutual information ranged from 0t/m to +0.8t/m in Sequence 7, Sequence 8 and Sequence 9.

5. Conclusion

We proposed to use negative mutual information for small bowel motility, which is different from traditional quantitative assessment by detecting the peristaltic frequency of a specific small bowel segment within MRI sequences. The simulation of the small bowel motility proves qualification for the proposed method. Experimental results demonstrate the accuracy of the proposed method, which outperforms the peristaltic times calculated by DBAM with intensity difference.

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